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Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application.

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LISTING OF CLAIMS

Claims 1-51 (Cancelled)

Claim 52 (Currently Amended) A method for determining coding features within a nucleic acid sequence ~~gene prediction~~ by determining a probability for each of one or more states for more than one ~~selected-examined~~ nucleotide in said nucleic acid sequence, comprising:

- a) determining an initial oligonucleotide probability for each of said states for an initial oligonucleotide in a window of a first ~~selected-examined~~ nucleotide;
- b) determining transition probabilities for each of said states for nucleotides within said window following said initial oligonucleotide;
- c) using said initial oligonucleotide probability and said transition probabilities to determine a plurality of window probabilities, wherein said plurality comprises a window probability corresponding to each of said states for said ~~selected-examined~~ nucleotide;
- d) applying a bias function to said plurality of window probabilities, to determine a probability for each of said states for said ~~selected-examined~~ nucleotide, wherein a the value being used in produced by said bias function is at least different in in at least one state within all of said from the other states for said ~~selected-examined~~ nucleotide; [[and,]]
- e) repeating steps a) through d) for each remaining ~~selected-examined~~ nucleotide in said nucleic acid sequence,

wherein said more than one ~~selected-examined~~ nucleotide are contiguous, and step e) is performed sequentially from said first ~~selected-examined~~ nucleotide to a last ~~selected-examined~~ nucleotide,

wherein said probability for each of said states for said more than one ~~selected-examined~~ nucleotide is determined using an inhomogeneous Markov model having eight states, wherein said eight states are: first reading frame positive strand (1+); second reading frame positive strand (2+); third reading frame positive strand (3+); first reading frame negative strand (1-); second reading frame negative

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strand (2-); third reading frame negative strand (3-); noncoding positive strand (N+); and noncoding negative strand (N-),

wherein said probability for each of said states for said more than one selected examined nucleotide is determined using the equation

$$P(f|\sigma) \text{ [[=]] } \frac{\phi(f) \cdot P_f \cdot P_f(S)}{\sum_{i \in \{1+, 2+, 3+, N+, 1-, 2-, 3-, N-\}} \phi(i) \cdot P_i \cdot P_i(S)}$$

$$P'(\sigma | S) = \frac{\phi(\sigma) \cdot P(\sigma) \cdot P(S | \sigma)}{\sum_i [\phi(i) \cdot P(i) \cdot P(S | i)]}$$

wherein i and σ are each one of said eight states,

wherein $P'(\sigma | S)$ is the probability of said inhomogeneous Markov model being in state σ after having examined nucleic acid sequence S ,

wherein $P(S | \sigma)$ is the probability of said inhomogeneous Markov model generating sequence S while in state σ ,

wherein $P(S | i)$ is the probability of said inhomogeneous Markov model generating sequence S while in state i ,

wherein $P(i)$ is the probability of said inhomogeneous Markov model being in state i , before having examined any sequence,

wherein $P(\sigma)$ is the probability of said inhomogeneous Markov model being in state σ , before having examined any sequence,

wherein $\phi(\sigma)$ is the bias function corresponding to said state σ , and

wherein $\phi(i)$ is the bias function corresponding to said state i ; and

f) providing said nucleic acid sequence as most probable states of said probability states for each of said states for each of more than one examined nucleotide wherein said most probable states demarcate said coding features of said nucleic acid sequence and providing said coding features as a translated protein sequence.

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Claims 53-55 (Cancelled)

Claim 56 (Previously presented) The method of claim 52, wherein said nucleic acid sequence is part of a longer nucleic acid sequence.

Claim 57 (Currently amended) The method of claim 52, wherein said examined ~~selected~~ nucleotide in said more than one examined ~~selected~~ nucleotide is the middle nucleotide in its own window.

Claims 58-59 (Cancelled)

Claim 60 (Currently amended) The method of claim 52, wherein the value being used in ~~produced by~~ said bias function is between 0.0 and 0.9, or greater than 1.1, in one or more of said states for said ~~selected~~ examined nucleotide.